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OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/805,311

DATE: 03/30/2001

TIME: 15:06:22

#

Input Set : A:\0961D Sequence Listing.txt

Output Set: N:\CRF3\03302001\I805311.raw

ENTERED

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4 <110> APPLICANT: Mahajan, Pramod B.
7 <120> TITLE OF INVENTION: Rad2/FEN-1 Orthologues and Uses
8   Thereof
10 <130> FILE REFERENCE: 0961D
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/805,311
C--> 12 <141> CURRENT FILING DATE: 2001-03-13
12 <150> PRIOR APPLICATION NUMBER: 09/426,557
13 <151> PRIOR FILING DATE: 1999-10-22
15 <150> PRIOR APPLICATION NUMBER: 60/112,332
16 <151> PRIOR FILING DATE: 1998-12-15
18 <160> NUMBER OF SEQ ID NOS: 10
20 <170> SOFTWARE: FastSEQ for Windows Version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1463
24 <212> TYPE: DNA
25 <213> ORGANISM: Zea mays
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (85)...(1221)
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33  cccgccacag ccgcccgcaga cgag atg ggc atc aag ggt ttg acg aaa ctg      111
34                                     Met Gly Ile Lys Gly Leu Thr Lys Leu
35                                     1               5
37  ctg gcg gac aat gcg ccc aag gcg atg aag gag cag aag ttc gag agc      159
38  Leu Ala Asp Asn Ala Pro Lys Ala Met Lys Glu Gln Lys Phe Glu Ser
39   10               15               20               25
41  tac ttc ggc cgc aaa atc gcc gtc gac gcc agc atg agc ata tac cag      207
42  Tyr Phe Gly Arg Lys Ile Ala Val Asp Ala Ser Met Ser Ile Tyr Gln
43               30               35               40
45  ttc ctg att gta gtt gga agg aca ggc atg gaa act ctc aca aat gaa      255
46  Phe Leu Ile Val Val Gly Arg Thr Gly Met Glu Thr Leu Thr Asn Glu
47               45               50               55
49  gct ggt gaa gtc act agt cat ttg caa gga atg ttc aac cgg aca ata      303
50  Ala Gly Glu Val Thr Ser His Leu Gln Gly Met Phe Asn Arg Thr Ile
51   60               65               70
53  aga tta ctg gaa gcg gga atc aag cca gtt tat gtt ttt gat ggc aag      351
54  Arg Leu Leu Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp Gly Lys
55   75               80               85
57  cct cct gat atg aag aaa caa gag ctt gct aaa aga tac tca aaa aga      399
58  Pro Pro Asp Met Lys Lys Gln Glu Leu Ala Lys Arg Tyr Ser Lys Arg
59   90               95               100               105
61  gat gat gca acc aaa gat ctg act gag gca gta gag gta gga gat aaa      447
62  Asp Asp Ala Thr Lys Asp Leu Thr Glu Ala Val Glu Val Gly Asp Lys
63               110               115               120
66  gat gcg att gaa aaa ttg agc aag agg act gta aag gtc aca agg caa      495
67  Asp Ala Ile Glu Lys Leu Ser Lys Arg Thr Val Lys Val Thr Arg Gln

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68					125				130				135				
70	cac	aac	gaa	gat	tgt	aaa	cgg	cta	tta	aga	ctt	atg	ggg	ggt	cct	ggt	543
71	His	Asn	Glu	Asp	Cys	Lys	Arg	Leu	Leu	Arg	Leu	Met	Gly	Val	Pro	Val	
72			140					145					150				
74	gta	gag	gca	cct	tct	gaa	gca	gaa	gca	gaa	tgt	gca	gcc	ctt	tgc	ata	591
75	Val	Glu	Ala	Pro	Ser	Glu	Ala	Glu	Ala	Glu	Cys	Ala	Ala	Leu	Cys	Ile	
76			155					160					165				
78	aac	gat	aag	gtg	ttc	gct	ggt	gct	tca	gaa	gat	atg	gac	tcc	ctt	act	639
79	Asn	Asp	Lys	Val	Phe	Ala	Val	Ala	Ser	Glu	Asp	Met	Asp	Ser	Leu	Thr	
80	170						175					180				185	
82	ttt	ggg	gct	cca	cgg	ttc	ctt	cgt	cat	tta	atg	gat	cca	agt	tcc	aag	687
83	Phe	Gly	Ala	Pro	Arg	Phe	Leu	Arg	His	Leu	Met	Asp	Pro	Ser	Ser	Lys	
84					190					195					200		
86	aaa	ata	cct	gtg	atg	gaa	ttt	gat	ggt	gcc	aag	ggt	ttg	gag	gag	ctt	735
87	Lys	Ile	Pro	Val	Met	Glu	Phe	Asp	Val	Ala	Lys	Val	Leu	Glu	Glu	Leu	
88				205					210				215				
90	gaa	ctc	acc	atg	gac	cag	ttc	att	gat	ttg	tgc	atc	ctg	tgt	gga	tgt	783
91	Glu	Leu	Thr	Met	Asp	Gln	Phe	Ile	Asp	Leu	Cys	Ile	Leu	Cys	Gly	Cys	
92			220					225					230				
94	gac	tat	tgt	gat	agc	atc	aaa	ggt	atc	ggg	ggg	caa	aca	gct	ctg	aaa	831
95	Asp	Tyr	Cys	Asp	Ser	Ile	Lys	Gly	Ile	Gly	Gly	Gln	Thr	Ala	Leu	Lys	
96		235					240					245					
98	ctt	att	cgt	caa	cat	ggg	tcc	ata	gaa	agc	atc	ttg	gag	aat	ctt	aat	879
99	Leu	Ile	Arg	Gln	His	Gly	Ser	Ile	Glu	Ser	Ile	Leu	Glu	Asn	Leu	Asn	
100	250					255					260					265	
102	aaa	gac	aga	tat	caa	att	cct	gag	gac	tgg	cct	tac	caa	gaa	gct	cga	927
103	Lys	Asp	Arg	Tyr	Gln	Ile	Pro	Glu	Asp	Trp	Pro	Tyr	Gln	Glu	Ala	Arg	
104				270						275				280			
106	cgc	ttg	ttc	aag	gag	cct	aat	gtc	aca	ttg	gat	att	cct	gag	cta	aaa	975
107	Arg	Leu	Phe	Lys	Glu	Pro	Asn	Val	Thr	Leu	Asp	Ile	Pro	Glu	Leu	Lys	
108				285					290				295				
110	tgg	act	gca	cct	gat	gag	gag	ggt	ctc	ata	agt	ttc	ctg	gta	aaa	gat	1023
111	Trp	Thr	Ala	Pro	Asp	Glu	Glu	Gly	Leu	Ile	Ser	Phe	Leu	Val	Lys	Asp	
112			300					305					310				
114	aat	ggt	ttc	aac	gaa	gat	cgg	gtg	aca	aag	gcc	ata	gag	aag	atc	aaa	1071
115	Asn	Gly	Phe	Asn	Glu	Asp	Arg	Val	Thr	Lys	Ala	Ile	Glu	Lys	Ile	Lys	
116		315					320					325					
118	tct	gcc	aag														

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137 gctcatgttt caagctgggg taagttagtt gtgtttgaag agattggtgt accaagtaac 1391
138 aaaacttata gctgtttttt acttcttgtc ctttgaagta aaaaaaaaaa aaaaaaaaaa 1451
139 aaaaaaaaaa aa 1463
141 <210> SEQ ID NO: 2
142 <211> LENGTH: 379
143 <212> TYPE: PRT
144 <213> ORGANISM: Zea mays
146 <400> SEQUENCE: 2
147 Met Gly Ile Lys Gly Leu Thr Lys Leu Leu Ala Asp Asn Ala Pro Lys
148 1 5 10 15
149 Ala Met Lys Glu Gln Lys Phe Glu Ser Tyr Phe Gly Arg Lys Ile Ala
150 20 25 30
151 Val Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Val Val Gly Arg
152 35 40 45
153 Thr Gly Met Glu Thr Leu Thr Asn Glu Ala Gly Glu Val Thr Ser His
154 50 55 60
155 Leu Gln Gly Met Phe Asn Arg Thr Ile Arg Leu Leu Glu Ala Gly Ile
156 65 70 75 80
157 Lys Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Asp Met Lys Lys Gln
158 85 90 95
159 Glu Leu Ala Lys Arg Tyr Ser Lys Arg Asp Asp Ala Thr Lys Asp Leu
160 100 105 110
161 Thr Glu Ala Val Glu Val Gly Asp Lys Asp Ala Ile Glu Lys Leu Ser
162 115 120 125
163 Lys Arg Thr Val Lys Val Thr Arg Gln His Asn Glu Asp Cys Lys Arg
164 130 135 140
165 Leu Leu Arg Leu Met Gly Val Pro Val Val Glu Ala Pro Ser Glu Ala
166 145 150 155 160
167 Glu Ala Glu Cys Ala Ala Leu Cys Ile Asn Asp Lys Val Phe Ala Val
168 165 170 175
169 Ala Ser Glu Asp Met Asp Ser Leu Thr Phe Gly Ala Pro Arg Phe Leu
170 180 185 190
171 Arg His Leu Met Asp Pro Ser Ser Lys Lys Ile Pro Val Met Glu Phe
172 195 200 205
173 Asp Val Ala Lys Val Leu Glu Glu Leu Glu Leu Thr Met Asp Gln Phe
174 210 215 220
175 Ile Asp Leu Cys Ile Leu Cys Gly Cys Asp Tyr Cys Asp Ser Ile Lys
176 225 230 235 240
177 Gly Ile Gly Gly Gln Thr Ala Leu Lys Leu Ile Arg Gln His Gly Ser
178 245 250 255
179 Ile Glu Ser Ile Leu Glu Asn Leu Asn Lys Asp Arg Tyr Gln Ile Pro
180 260 265 270
181 Glu Asp Trp Pro Tyr Gln Glu Ala Arg Arg Leu Phe Lys Glu Pro Asn
182 275 280 285
183 Val Thr Leu Asp Ile Pro Glu Leu Lys Trp Thr Ala Pro Asp Glu Glu
184 290 295 300
185 Gly Leu Ile Ser Phe Leu Val Lys Asp Asn Gly Phe Asn Glu Asp Arg
186 305 310 315 320
187 Val Thr Lys Ala Ile Glu Lys Ile Lys Ser Ala Lys Asn Lys Ser Ser

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188          325          330          335
190  Gln Gly Arg Leu Glu Ser Phe Phe Lys Pro Thr Ala Thr Thr Ser Ala
191          340          345          350
192  Pro Leu Lys Arg Lys Glu Thr Ser Asp Lys Thr Ser Lys Ala Ala Ala
193          355          360          365
194  Asn Lys Lys Thr Lys Ala Gly Gly Lys Lys Lys
195          370          375
197 <210> SEQ ID NO: 3
198 <211> LENGTH: 1541
199 <212> TYPE: DNA
200 <213> ORGANISM: Zea mays
202 <220> FEATURE:
203 <221> NAME/KEY: CDS
204 <222> LOCATION: (79)...(1215)
206 <400> SEQUENCE: 3
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208  acagccgccg cagacgag atg ggc atc aag ggt ttg acg aaa ctg ctg gcg      111
209          Met Gly Ile Lys Gly Leu Thr Lys Leu Leu Ala
210          1          5          10
212  gac aat gcg ccc aag gcg atg aag gag cag aag ttc gag agc tac ttc      159
213  Asp Asn Ala Pro Lys Ala Met Lys Glu Gln Lys Phe Glu Ser Tyr Phe
214          15          20          25
216  ggc cgc aaa atc gcc gtc gac gcc agc atg agc ata tac cag ttc ctg      207
217  Gly Arg Lys Ile Ala Val Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu
218          30          35          40
220  att gta gtt gga agg aca ggc atg gaa act ctc aca aat gaa gct ggt      255
221  Ile Val Val Gly Arg Thr Gly Met Glu Thr Leu Thr Asn Glu Ala Gly
222          45          50          55
224  gaa gtc act agt cat ttg caa gga atg ttc aac cgg aca ata aga tta      303
225  Glu Val Thr Ser His Leu Gln Gly Met Phe Asn Arg Thr Ile Arg Leu
226          60          65          70          75
228  ctg gaa gcg gga atc aag cca gtt tat gtt ttt gat ggc aag cct cct      351
229  Leu Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp Gly Lys Pro Pro
230          80          85          90
232  gat atg aag aaa caa gag ctt gct aaa aga tac tca aaa aga gat gat      399
233  Asp Met Lys Lys Gln Glu Leu Ala Lys Arg Tyr Ser Lys Arg Asp Asp
234          95          100          105
236  gca acc aaa gat ctg act gag gca gta gag gta gga gat aaa gat gcg      447
237  Ala Thr Lys Asp Leu Thr Glu Ala Val Glu Val Gly Asp Lys Asp Ala
238          110          115          120
240  att gaa aaa ttg agc aag agg act gta aag gtc aca agg caa cac aac      495
241  Ile Glu Lys Leu Ser Lys Arg Thr Val Lys Val Thr Arg Gln His Asn
242          125          130          135
244  gaa gat tgt aaa cgg cta tta aga ctt atg ggg gtt cct gtt gta gag      543
245  Glu Asp Cys Lys Arg Leu Leu Arg Leu Met Gly Val Pro Val Val Glu
246          140          145          150          155
248  gca cct tct gaa gca gaa gca gaa tgt gca gcc ctt tgc ata aac gat      591
249  Ala Pro Ser Glu Ala Glu Ala Glu Cys Ala Ala Leu Cys Ile Asn Asp
250          160          165          170

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252 aag gtg ttc gct gtt gct tca gaa gat atg gac tcc ctt act ttt ggg      639
253 Lys Val Phe Ala Val Ala Ser Glu Asp Met Asp Ser Leu Thr Phe Gly
254      175      180      185
256 gct cca cgg ttc ctt cgt cat tta atg gat cca agt tcc aag aaa ata      687
257 Ala Pro Arg Phe Leu Arg His Leu Met Asp Pro Ser Ser Lys Lys Ile
258      190      195      200
260 cct gtg atg gaa ttt gat gtt gcc aag gtt ttg gag gag ctt gaa ctc      735
261 Pro Val Met Glu Phe Asp Val Ala Lys Val Leu Glu Glu Leu Glu Leu
262      205      210      215
264 acc atg gac cag ttc att gat ttg tgc atc ctg tgt gga tgt gac tat      783
265 Thr Met Asp Gln Phe Ile Asp Leu Cys Ile Leu Cys Gly Cys Asp Tyr
266      220      225      230      235
268 tgt gat agc atc aaa ggt atc ggg ggg caa aca gct ctg aaa ctt att      831
269 Cys Asp Ser Ile Lys Gly Ile Gly Gly Gln Thr Ala Leu Lys Leu Ile
270      240      245      250
272 cgt caa cat ggg tcc ata gaa agc atc ttg gag aat ctt aat aaa gac      879
273 Arg Gln His Gly Ser Ile Glu Ser Ile Leu Glu Asn Leu Asn Lys Asp
274      255      260      265
276 aga tat caa att cct gag gac tgg cct tac caa gaa gct cga cgc ttg      927
277 Arg Tyr Gln Ile Pro Glu Asp Trp Pro Tyr Gln Glu Ala Arg Arg Leu
278      270      275      280
280 ttc aag gag cct aat gtc aca ttg gat att cct gag cta aaa tgg act      975
281 Phe Lys Glu Pro Asn Val Thr Leu Asp Ile Pro Glu Leu Lys Trp Thr
282      285      290      295
284 gca cct gat gag gag ggt ctc ata agt ttc ctg gta aaa gat aat ggt      1023
285 Ala Pro Asp Glu Glu Gly Leu Ile Ser Phe Leu Val Lys Asp Asn Gly
286      300      305      310      315
288 ttc aac gaa gat cgg gtg aga aag gcc ata gag aag atc aaa tct gcc      1071
289 Phe Asn Glu Asp Arg Val Arg Lys Ala Ile Glu Lys Ile Lys Ser Ala
290      320      325      330
292 aag aat aaa tcg tcg caa gga aga ctc gag tcc ttt ttc aag cca act      1119
293 Lys Asn Lys Ser Ser Gln Gly Arg Leu Glu Ser Phe Phe Lys Pro Thr
294      335      340      345
296 gcc acc aca tca gca ccg cta aaa cgg aag gag act tcg gat aaa aca      1167
297 Ala Thr Thr Ser Ala Pro Leu Lys Arg Lys Glu Thr Ser Asp Lys Thr
298      350      355      360
300 agc aag gca gct gcg aac aag aaa aca aag gct ggt gga aag aag aaa      1215
301 Ser Lys Ala Ala Ala Asn Lys Lys Thr Lys Ala Gly Gly Lys Lys Lys
302      365      370      375
304 taatcttgga tgcttgatgt acaactacga ctacgaaagc agcgggtggcg tgatcacttc      1275
305 gcttagatta ttttaactccc tgttttaact cagagctttg gtaaaagttt gctcatgttt      1335
306 caagctgggg taagttagtt gtgtttgaag agattgggtgt accaagtaac aaaacttata      1395
307 gctgtttttt acttctgttc ctttgaagta tgtatgccag tcctcgtcct tttaagtata      1455
308 tgtgttgcaa caaaaattta aggccttggt ttgatgcata ggctcacttt aagatttagt      1515
309 ttaaatttca aaaaaaaaaa aaaaaa      1541
314 <210> SEQ ID NO: 4
315 <211> LENGTH: 379
316 <212> TYPE: PRT
317 <213> ORGANISM: Zea mays

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VERIFICATION SUMMARY

DATE: 03/30/2001

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Input Set : A:\0961D Sequence Listing.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date